



US-1380
SEQUENCE LISTING

<110> IZUI, Masako
SUGIMOTO, Masakazu
KURAHASHI, Osamu
NAKAMATSU, TSUYOSHI

<120> DNA Encoding Sucrose PTS Enzyme II

<130> 217677US0PCT

<140> US 10/019,284
<141> 2002-01-02

<150> JP 11-189512
<151> 1999-07-02

<160> 21

<170> PatentIn Ver. 2.0

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tctgcagttt ttaagttatg catcatcagc ttggaaaggct gaggtaattc agtagacctg 240
caacagcagg cctcaagttc gaagataattt aaccttagatc cgttagacata agacatcata 300
cgtcctatgc ttgctggaaag gaaccaaata acctcagaaa gatggcagaa gtgggcatt 360
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US-1380

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gataatacag	ccattgagat	aactcgagg	gatggacagg	tttcattcgc	tttccgggc	3600
cttcaaaagg	gacacttattt	agagataatg	catataaaa	ggtctttgt	ggcgaattgt	3660
acaaataactt	cgcaaaatcc	cttgcattca	cacaaataaa	caggttaat	attgttttagc	3720
ttttgaacaa	acattcatgt	ctgaatattt	ttgtttctt	ccggttaagg	agaaattc	3778
atg gac cat aag gac ctc gcg caa cgc atc ctg cgc gac att ggc ggc						3826
Met Asp His Lys Asp Leu Ala Gln Arg Ile Leu Arg Asp Ile Gly Gly						
1	5	10	15			
gaa gac aac att gtc	gcc gcc gca	cac tgt gca	acg cgt tta	cgc ctc		3874
Glu Asp Asn Ile Val	Ala Ala Ala	His Cys Ala	Thr Arg Leu	Arg Leu		
20	25	30				
gtg ctc aaa gac acc aag gat	gtg gat cgc caa	agt ctg gat	gat gat gat			3922
Val Leu Lys Asp Thr Lys	Asp Val Asp Arg	Gln Ser Leu	Asp Asp Asp			
35	40	45				
cca gat ctg aaa ggc acc	ttt gaa act ggc	ggc atg ttc	cag atc atc			3970
Pro Asp Leu Lys Gly	Thr Phe Glu Thr	Gly Gly Met	Phe Gln Ile Ile			
50	55	60				
gtc ggg cca ggc gat	gtg gat cat gtt	ttc aaa gaa	ctc gat gac	gca		4018
Val Gly Pro Gly Asp Val	Asp His Val	Phe Lys Glu	Leu Asp Asp	Ala		
65	70	75	80			
acc tcc aaa gac atc	gct gtg tcc	aca gag cag	ctc aaa gat	gtt gtg		4066

US-1380

Thr Ser Lys Asp Ile Ala Val Ser Thr Glu Gln Leu Lys Asp Val Val	85	90	95	
Ala Asn Asn Ala Asn Trp Phe Ser Arg Ala Val Lys Val Leu Ala Asp	100	105	110	4114
Ile Phe Val Pro Leu Ile Pro Ile Leu Val Gly Gly Leu Leu Met	115	120	125	4162
gct atc aac aat gtc ttg gtt gtc gat ctc gtc ggt ccg caa tca	130	135	140	4210
Ala Ile Asn Asn Val Leu Val Ala Gln Asp Leu Phe Gly Pro Gln Ser				
ctg gtg gag atg ttc cct cag atc agc ggt gtt gct gag atg atc aac	145	150	155	4258
Leu Val Glu Met Phe Pro Gln Ile Ser Gly Val Ala Glu Met Ile Asn				
ctg atg gca tct gcg ccg ttc gcg ttc ttg cca gtg ttg gtt ggt ttc	165	170	175	4306
Leu Met Ala Ser Ala Pro Phe Ala Phe Leu Pro Val Leu Val Gly Phe				
acc gca acc aag cgt ttc ggt ggc aat gag ttc ctg ggc gcc ggc att	180	185	190	4354
Thr Ala Thr Lys Arg Phe Gly Gly Asn Glu Phe Leu Gly Ala Gly Ile				
ggt atg gcg atg gtg ttc cca acc ctg gtt aac ggc tac gac gtg gcc	195	200	205	4402
Gly Met Ala Met Val Phe Pro Thr Leu Val Asn Gly Tyr Asp Val Ala				
gcc acc atg acc gcg ggc gaa atg cca atg tgg tcc ctg ttt ggt ttg	210	215	220	4450
Ala Thr Met Thr Ala Gly Glu Met Pro Met Trp Ser Leu Phe Gly Leu				
gat gtt gct caa gct ggt tac cag ggc acc gtg ctt cct gtg ctg gtg	225	230	235	4498
Asp Val Ala Gln Ala Gly Tyr Gln Gly Thr Val Leu Pro Val Leu Val				
gtc tct tgg att ctg gca acg atc gag aag ttc ctg cac aag cga ctc	240	245	250	4546
Val Ser Trp Ile Leu Ala Thr Ile Glu Lys Phe Leu His Lys Arg Leu				
atg ggc act gca gac ttc ctg atc acc cca gtg ttg act ctg ctg ctc	260	265	270	4594
Met Gly Thr Ala Asp Phe Leu Ile Thr Pro Val Leu Thr Leu Leu Leu				
acc ggc ttc ctt acg ttc att gct att ggt cca gca atg cgc tgg gtg	275	280	285	4642
Thr Gly Phe Leu Thr Phe Ile Ala Ile Gly Pro Ala Met Arg Trp Val				
ggt gac ttg ctg gca cac ggt ctg cag gga ctc tat gat ttc ggt ggt	290	295	300	4690
Gly Asp Leu Leu Ala His Gly Leu Gln Gly Leu Tyr Asp Phe Gly Gly				
cca gtc ggc ggt ctg ctt ttc ggt ctg gtc tac tca cca atc gtt atc	305	310	315	4738
Pro Val Gly Gly Leu Leu Phe Gly Leu Val Tyr Ser Pro Ile Val Ile				
act ggt ctg cac cag tcc ttc ccg cca att gag ctg gag ctg ttc aac	320	325	330	4786
Thr Gly Leu His Gln Ser Phe Pro Pro Ile Glu Leu Glu Leu Phe Asn				
cag ggt gga tcc ttc atc ttc gca acc gca tcc atg gcc aat atc gcg	340	345	350	4834
Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser Met Ala Asn Ile Ala				
cag ggt gca gca tgt ttg gca gtg ttc ttc cta gcg aag agt gaa aag	355	360	365	4882
Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu Ala Lys Ser Glu Lys				
ctc aag ggc ctt gca ggt gct tca ggt gtc tcc gct gtt ctt ggt att	370	375	380	4930
Leu Lys Gly Leu Ala Gly Ala Ser Gly Val Ser Ala Val Leu Gly Ile				

US-1380

370	375	380	
aca gag cct gcg atc ttc ggt gtg aac ctt cgc ctg cgc tgg ccg ttc			4978
Thr Glu Pro Ala Ile Phe Gly Val Asn Leu Arg Leu Arg Trp Pro Phe			
385	390	395	400
tac att ggt atc ggt acc gca gct atc ggt ggc gct ttg att gca ctc			5026
Tyr Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly Ala Leu Ile Ala Leu			
405	410	415	
ttt gat atc aag gca gtt gcg ttg ggc gct gca ggt ttc ttg ggt gtt			5074
Phe Asp Ile Lys Ala Val Ala Leu Gly Ala Ala Gly Phe Leu Gly Val			
420	425	430	
gtt tct att gat gct cca gat atg gtc atg ttc ttg gtt tgc gcg gta			5122
Val Ser Ile Asp Ala Pro Asp Met Val Met Phe Leu Val Cys Ala Val			
435	440	445	
gtt acc ttt gtc atc gca ttc ggc gca gcg att gct tat ggc ctt tac			5170
Val Thr Phe Val Ile Ala Phe Gly Ala Ala Ile Ala Tyr Gly Leu Tyr			
450	455	460	
ttg gtt cgc cgc aac ggc agc att gat cca gat gca acc gct gct cca			5218
Leu Val Arg Arg Asn Gly Ser Ile Asp Pro Asp Ala Thr Ala Ala Pro			
465	470	475	480
gtg cct gca gga acg acc aaa gcc gaa gca gaa gca ccc gca gaa ttt			5266
Val Pro Ala Gly Thr Thr Lys Ala Glu Ala Glu Ala Pro Ala Glu Phe			
485	490	495	
tca aac gat tcc acc atc atc cag gca cct ttg acc ggt gaa gct atc			5314
Ser Asn Asp Ser Thr Ile Ile Gln Ala Pro Leu Thr Gly Glu Ala Ile			
500	505	510	
gca ctg agc agc gtc agc gat gcc atg ttt gcc agc gga aag ctt ggc			5362
Ala Leu Ser Ser Val Ser Asp Ala Met Phe Ala Ser Gly Lys Leu Gly			
515	520	525	
tca ggt gtt gcg atc gtc ccc acc aag ggg cag ctg gtt tca cca gtg			5410
Ser Gly Val Ala Ile Val Pro Thr Lys Gly Gln Leu Val Ser Pro Val			
530	535	540	
agc gga aag atc gtc gtg gcc ttc cca tct ggt cac gct ttc gca gtc			5458
Ser Gly Lys Ile Val Val Ala Phe Pro Ser Gly His Ala Phe Ala Val			
545	550	555	560
cgc act aag gct gag gat ggt tcc aat gtg gat atc ttg atg cac att			5506
Arg Thr Lys Ala Glu Asp Gly Ser Asn Val Asp Ile Leu Met His Ile			
565	570	575	
ggt ttc gac acc gta aac ctc aac ggc acg cac ttt aac ccg ctg aag			5554
Gly Phe Asp Thr Val Asn Leu Asn Gly Thr His Phe Asn Pro Leu Lys			
580	585	590	
aag cag ggc gat gaa gtc aaa gca ggg gag ctg ctg tgt gaa ttc gat			5602
Lys Gln Gly Asp Glu Val Lys Ala Gly Glu Leu Leu Cys Glu Phe Asp			
595	600	605	
att gat gcc att aag gct gca ggt tat gag gta acc acg ccg att gtt			5650
Ile Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val Thr Thr Pro Ile Val			
610	615	620	
gtt tcg aat tac aag aaa acc gga cct gta aac act tac ggt ttg ggc			5698
Val Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn Thr Tyr Gly Leu Gly			
625	630	635	640
gaa att gaa gcg gga gcc aac ctg ctc aac gtc gca aag aaa gaa gcg			5746
Glu Ile Glu Ala Gly Ala Asn Leu Leu Asn Val Ala Lys Lys Glu Ala			
645	650	655	
gtg cca gca aca cca taagttgaaa ccttgagtgt tcgcacacag gtttagactag			5801
Val Pro Ala Thr Pro			
660			

US-1380

gggacgtgac tctacgcac tttgacaccg gtacccgtac gcttcagat tttaaacctg 5861
 ttcaaccagg tcatgcctcg gtgtacctgt gtggccac cccgcaatct tcacccaca 5921
 ttggacatgt tcgttcagca gtagcgttg atatttgcg ccgctgaa 5969

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<211> 661

<212> PRT

<213> Brevibacterium lactofermentum

<400> 2

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 20 25 30
 Val Leu Lys Asp Thr Lys Asp Val Asp Arg Gln Ser Leu Asp Asp Asp
 35 40 45
 Pro Asp Leu Lys Gly Thr Phe Glu Thr Gly Gly Met Phe Gln Ile Ile
 50 55 60
 Val Gly Pro Gly Asp Val Asp His Val Phe Lys Glu Leu Asp Asp Ala
 65 70 75 80
 Thr Ser Lys Asp Ile Ala Val Ser Thr Glu Gln Leu Lys Asp Val Val
 85 90 95
 Ala Asn Asn Ala Asn Trp Phe Ser Arg Ala Val Lys Val Leu Ala Asp
 100 105 110
 Ile Phe Val Pro Leu Ile Pro Ile Leu Val Gly Gly Leu Leu Met
 115 120 125
 Ala Ile Asn Asn Val Leu Val Ala Gln Asp Leu Phe Gly Pro Gln Ser
 130 135 140
 Leu Val Glu Met Phe Pro Gln Ile Ser Gly Val Ala Glu Met Ile Asn
 145 150 155 160
 Leu Met Ala Ser Ala Pro Phe Ala Phe Leu Pro Val Leu Val Gly Phe
 165 170 175
 Thr Ala Thr Lys Arg Phe Gly Gly Asn Glu Phe Leu Gly Ala Gly Ile
 180 185 190
 Gly Met Ala Met Val Phe Pro Thr Leu Val Asn Gly Tyr Asp Val Ala
 195 200 205
 Ala Thr Met Thr Ala Gly Glu Met Pro Met Trp Ser Leu Phe Gly Leu
 210 215 220
 Asp Val Ala Gln Ala Gly Tyr Gln Gly Thr Val Leu Pro Val Leu Val
 225 230 235 240
 Val Ser Trp Ile Leu Ala Thr Ile Glu Lys Phe Leu His Lys Arg Leu
 245 250 255
 Met Gly Thr Ala Asp Phe Leu Ile Thr Pro Val Leu Thr Leu Leu Leu
 260 265 270
 Thr Gly Phe Leu Thr Phe Ile Ala Ile Gly Pro Ala Met Arg Trp Val
 275 280 285
 Gly Asp Leu Leu Ala His Gly Leu Gln Gly Leu Tyr Asp Phe Gly Gly
 290 295 300
 Pro Val Gly Gly Leu Leu Phe Gly Leu Val Tyr Ser Pro Ile Val Ile
 305 310 315 320
 Thr Gly Leu His Gln Ser Phe Pro Pro Ile Glu Leu Glu Leu Phe Asn
 325 330 335
 Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser Met Ala Asn Ile Ala
 340 345 350
 Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu Ala Lys Ser Glu Lys

US-1380

Leu	Lys	Gly	Leu	Ala	Gly	Ala	Ser	Gly	Val	Ser	Ala	Val	Leu	Gly	Ile
355			360								365				
370			375								380				
Thr	Glu	Pro	Ala	Ile	Phe	Gly	Val	Asn	Leu	Arg	Leu	Arg	Trp	Pro	Phe
385					390				395					400	
Tyr	Ile	Gly	Ile	Gly	Thr	Ala	Ala	Ile	Gly	Gly	Ala	Leu	Ile	Ala	Leu
									405		410			415	
Phe	Asp	Ile	Lys	Ala	Val	Ala	Leu	Gly	Ala	Ala	Gly	Phe	Leu	Gly	Val
								420		425			430		
Val	Ser	Ile	Asp	Ala	Pro	Asp	Met	Val	Met	Phe	Leu	Val	Cys	Ala	Val
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Val	Thr	Phe	Val	Ile	Ala	Phe	Gly	Ala	Ala	Ile	Ala	Tyr	Gly	Leu	Tyr
							450		455			460			
Leu	Val	Arg	Arg	Asn	Gly	Ser	Ile	Asp	Pro	Asp	Ala	Thr	Ala	Ala	Pro
465					470					475					480
Val	Pro	Ala	Gly	Thr	Thr	Lys	Ala	Glu	Ala	Glu	Ala	Pro	Ala	Glu	Phe
							485		490			495			
Ser	Asn	Asp	Ser	Thr	Ile	Ile	Gln	Ala	Pro	Leu	Thr	Gly	Glu	Ala	Ile
							500		505			510			
Ala	Leu	Ser	Ser	Val	Ser	Asp	Ala	Met	Phe	Ala	Ser	Gly	Lys	Leu	Gly
							515		520			525			
Ser	Gly	Val	Ala	Ile	Val	Pro	Thr	Lys	Gly	Gln	Leu	Val	Ser	Pro	Val
							530		535			540			
Ser	Gly	Lys	Ile	Val	Val	Ala	Phe	Pro	Ser	Gly	His	Ala	Phe	Ala	Val
545							550			555					560
Arg	Thr	Lys	Ala	Glu	Asp	Gly	Ser	Asn	Val	Asp	Ile	Leu	Met	His	Ile
							565			570			575		
Gly	Phe	Asp	Thr	Val	Asn	Leu	Asn	Gly	Thr	His	Phe	Asn	Pro	Leu	Lys
							580			585			590		
Lys	Gln	Gly	Asp	Glu	Val	Lys	Ala	Gly	Glu	Leu	Leu	Cys	Glu	Phe	Asp
							595			600			605		
Ile	Asp	Ala	Ile	Lys	Ala	Ala	Gly	Tyr	Glu	Val	Thr	Thr	Pro	Ile	Val
							610			615			620		
Val	Ser	Asn	Tyr	Lys	Lys	Thr	Gly	Pro	Val	Asn	Thr	Tyr	Gly	Leu	Gly
625							630			635					640
Glu	Ile	Glu	Ala	Gly	Ala	Asn	Leu	Leu	Asn	Val	Ala	Lys	Lys	Glu	Ala
							645			650			655		
Val	Pro	Ala	Thr	Pro											
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<210> 3
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Sau3AI cassette

<220>
 <221> misc_feature
 <222> (44)
 <223> complementary strand extends a single strand having
 a sequence of 3'-ctag-5' at this position in the
 direction of 5' from 3'

US-1380

<400> 3 gtacatattg tcgttagaac gcgtaatacg actcactata ggga	44
<210> 4 <211> 47 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: EcoRI cassette	
<220> <221> misc_feature <222> (47) <223> complementary strand extends a single strand having a sequence of 3'-ttaa-5' at this position in the direction of 5' from 3'	
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<210> 5 <211> 46 <212> DNA <213> Artificial Sequence	
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<210> 6 <211> 51 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PstI cassette <220> <221> misc_feature <222> (48)..(51) <223> complementary strand does not exist	
<400> 6 gtacatattg tcgttagaac gcgtaatacg actcactata gggagactgc a	51
<210> 7	

US-1380

<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SalI cassette

<220>
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<222> (47)
<223> complementary strand extends a single strand having a sequence of 3'-agct-5' at this position in the direction of 5' from 3'

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gtacatattg tcgttagaac gcgtaatacg actcactata gggagag 47

<210> 8
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: XbaI cassette

<220>
<221> misc_feature
<222> (47)
<223> complementary strand extends a single strand having a sequence of 3'-gatc-5' at this position in the direction of 5' from 3'

<400> 8
gtacatattg tcgttagaac gcgtaatacg actcactata gggagat 47

<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 9
cgtctgcga ggattcagcg agctg 25

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for PCR

<400> 10

US-1380

25

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<210> 11

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for PCR

<400> 11

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23

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer for PCR

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25

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<213> Artificial Sequence

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US-1380

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US-1380

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